

ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60
 ATGTGCTTTT TAAATTGGCC TCGTGACCC GCCCACTTGG TGTAAAGAA GAACGGGCA 120
 AAGGGAGGCG CTGAAGGACC TCCACAGAG TGTGAGCAG ACTGCTTCAG CAACAAAGCC 180
 TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC 231
 Met Ala Thr Ser Trp Gly Ala Val Phe
 1 5

ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG 279
 Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
 10 15 20 25

CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT 327
 Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
 30 35 40

GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT 375
 Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
 45 50 55

GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG 423
 Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
 60 65 70

CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT 471
 Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu
 75 80 85

TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG 519
 Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
 90 95 100 105

CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG 567
 Leu Thr Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg
 110 115 120

ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG 615
 Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu
 125 130 135

CAG AAA GCC CAG GCT GCT CTC CTC GAG GTA GAG GAG ATC TTC AAG AAT 663
 Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn
 140 145 150

TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC 711
 Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser
 155 160 165

TAT GAA GGC ATA CTA GCC TGG GTT ATC GTG AAC TTT CTA ACA GGT CAG 759
 Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln
 170 175 180 185

CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT 807
 Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly
 190 195 200

GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA 855
 Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu
 205 210 215

CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT 903
 Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr
 220 225 230

Fig. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA CTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GGC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCTTTTGGGA	1749
TTCTTTGTAC	AGAGTCTTGC	AAAGGAAAAA	AGACAAAACC	TTTGGAACTC	CATGCTAGAT	1809
TGGAGTTCA	GAGACAGTC	CCTGGGGACC	AAAGAACAAAT	CTCGTTTCAA	CCCTGGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTCG	TTATAAGCTG	ATTTACTGAA	ATCCCAATAC	1929
CCATCAATGC	TGTTAATTTT	TTTCTTCCTA	CCCTTATTAC	ATTCCCTACC	CTAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTG	CTTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATTT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

Fig. 1 (cont'd.)

FIG. 2

ACR I

CD39
ratCD39
CD39L1
chickATPase
pcaNTFase
potKROP1
yGDA1
mNTFase
hCD39L2
celegane
v71KD



ACR II

CD39
retCD39
CD39L1
chickATPase
pseATPase
potRNOF1
yGDA1
mATPase
hCD39L2
calsegane
v71ED



ACR III

CD39
retCD39
CD39L1
chickATPase
pearATPase
potKHOP1
YGD1
mATPase
hCD39L2
celegans
y71KD



ACR IV

F16.3

GTGGGGTGGT ATCCGCGGGG TGGAGGCGGG GGTGGCGCGG GCCGGGCGGG GGGAGCCCAA	60
AAGACCGGCT GCCGCGTGGT CCGCGGAAAA GGGCACTGGT CTCCCTCCCT CTGGCGGAGC	120
CGCGCGTGCA TGGAAATGGGC TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA	180
AAAACGAGCT ACATTTTTC ACGAGCCGAG CACGGTCCTT GGCAAAACAG G ATG AGA	237
Met Arg	
1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CGG GGG CGG CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GGT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TGG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
180 185 190 200	
GAT GAA GGC GTT TGG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTGAC CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTG ATAAACCCCT CTGTCCTGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACCTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGACCTG GGCCCTGCTC 460 465 470 475 480 485 490	1697 1757 1817

Fig. 4 (cont'd.)

AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAACC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCECA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	CTGCGATGGG	AGTCTTGTCT	CCCAGCCTGT	CAGTTTCTTC	1997
CCGAGGGCAG	AGCTCCCCCTT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCTCTGGCTG	2057
CTCTGGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCGGGAC	AGTAGSTCTG	GCGGGCACCA	2117
CTGGGAATCT	TGGACTTGAG	TGTGTTTGTCT	CTTCTTTGGG	TATGAATGTG	TSAGTTCACC	2177
CAGAGGCGCTG	CTCTCCTCAC	ACATTGTGTG	GTTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGGC	2297
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGCTCTCTG	TCGTGCGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCCTAGCCA	GGGCCATGTC	TTAGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTTG	CTCGGGCCAC	2537
CATCCGCCCA	CCTCGGGCTG	ACCCACCTTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCGGTG	2597
TACCTCTGCTC	AGTGTGGGCT	CAGTGTGGGG	GCTGAGCCTC	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTTCACAGGG	2717
GCTTCTCCTT	CAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA		2762

Fig. 4 (cont'd)

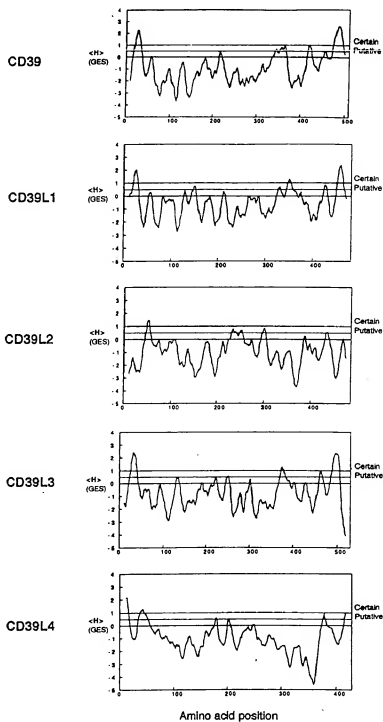


FIG. 5

ACCCACGCGT CTGGCCGCGG GCCGCTCTG CGGCAGCGCT AGTCGCTTC TCAGAATCGG	60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT	112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys	
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC	160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC	208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT	256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA	304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Tyr Gly Asn Asn Pro	
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA CTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC CTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	

Fig. 6

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Ser Gln Leu Pro Leu Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC	1703
Asp His Ala Val Asp Ser Asp	
525	
TGCTTAGAGT CAGCCTGGGT GGCACGAGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA	1763
TACAACTAAC TAAAAATCAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTCTGCCCAC	1823
AGCACTCTTT GAGGCATCCC TTGGCTATTCT TGTGCATATT GTTCTTCAGA GACCTCACTA	1883
CCCACTTGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA	1943
TATTAGATTG CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAAATG TGAAGAATTG	2003
ACCTCAGGGC TCAGTTTCCA TTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA	2063
AGCATTTCCG CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT	2123
TTCTTTGAGC AATCTCGTAA GCAGTGAACC CCTCAGATC AGTAGAATAT AGTATCTGGG	2183
GGAGAGACT TACTTCTTTC AGGGCAGAG CCKAGCCAG GCTTTCTGCA TACAGTAGA	2243
TCCCGAAGCA CAGAGACATA AAAAAGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG	2303
GAATTTCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGC ATCATCCTCA	2363
TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT	2423
GCATTCCAGA TTTTACTGCC TTTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTTCCATT	2483
GTTATCATGG TGTATATATT TTTGTCACCA TTCCCAAGG TATACTTGAT GTTGTCTAG	2543
AACGACATC CTACTCTATG ATTACTTAAC CAATTACTTT CCAGATCAT AGACTCTCT	2603
CATAGTAGT CATAGGTCCT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC	2663
TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAAATG CTACAACTA AAAATCAGCA	2723
TTATTTTATA TTGCTGTTTC TTAGCTGAAT ATGGAATATA GAACATATTAT TTTATTTTGA	2783
AAAAAAAAAA AAAA	2797

Fig. 6 (cont'd)

GGCGCGCGGT	TTTCTTGT	CTGTGTCAC	AAAGAAATGT	GGAGTGTCTT	GGCTGAATCC	60
TCATACGAGC	AAGATCAITA	TGGTGTGTT	AGGTAGGACT	TGTATCCAGA	TGTAAGGTG	120
AAAAAGTCAT	ATAATAAAGG	AACCAAGGAG	AAAAATCAGA	AGGAAAGAAA	AAATTCGCTC	180
TGCAGGTGTG	CGAGCAGGAT	TGCTTCTGCA	ACAAAAGCCT	CCACCCAGCC	ACATCTTGGG	240
AAAAGA ATG	GCC ACT TCT	TGG GGC ACA	GTC TTT TTC	ATG CTG	CTG GTA	288
Met Ala Thr Ser	Trp Gly Thr Val	Phe Phe Met Leu	Val Val			
1	5	10				
TCC TGT GTT TGC AGC GCT	GTC TCC CAC AGG AAC	CAG CAG ACT TGG TTT				336
Ser Cys Val Cys Ser	Ala Val Ser His Arg	Asn Gln Gln Thr	Trp Phe			
15	20	25	30			
GAG GGT ATC TTC CTG TCT	TCC ATG TGC CCC ATC	AAT GTC AGC GCC AGC				384
Glu Gly Ile Phe Leu Ser	Ser Met Cys Pro Ile	Asn Val Ser Ala Ser				
35	40	45				
ACC TTG TAT GGA ATT ATG	TTT GAT GCA GGG AGC	ACT GGA ACT CGA ATT				432
Thr Leu Tyr Gly Ile Met	Phe Asp Ala Gly Ser	Thr Gly Thr Arg Ile				
50	55	60				
CAT GTT TAC ACC TTT GTG	CAG AAA ATG CCA GGA	CAG CTT CCA ATT CTA				480
His Val Tyr Thr Phe Val	Gln Lys Met Pro Gly	Gln Leu Pro Ile Leu				
65	70	75				
GAA GGG GAA GTT TTT GAT	TCT GTG AAG CCA GGA	CTT TCT GCT TTT GTA				528
Glu Gly Glu Val Phe Asp	Ser Val Lys Pro Gly	Leu Ser Ala Phe Val				
80	85	90				
GAT CAA CCT AAG CAG GGT	GCT GAG ACC GTT CAA	GGG CTC TTA GAG GTG				576
Asp Gln Pro Lys Gln Gly	Ala Glu Thr Val Gln	Gly Leu Leu Glu Val				
95	100	105				
GCC AAA GAC TCA ATC CCC	CGA AGT CAC TGG AAA	AAG ACC CCA GTG GTC				624
Ala Lys Asp Ser Ile Pro	Arg Ser His Trp Lys	Lys Thr Pro Val Val				
115	120	125				
CTA AAG GCA ACA GCA GGA	CTA CGC TTA CTG CCA	GAA CAC AAA GCC AAG				672
Leu Lys Ala Thr Ala Gly	Leu Arg Leu Pro Glu	His Lys Ala Lys				
130	135	140				
GCT CTG CTC TTT GAG GTA	AAG GAG ATC TTC AGG	AAG TCA CCT TTC CTG				720
Ala Leu Leu Phe Glu Val	Lys Glu Ile Phe Arg	Lys Ser Pro Phe Leu				
145	150	155				
GTA CCA AAG GGC AGT GTT	AGC ATC ATG GAT GGA	TCC GAC GAA GGC ATA				768
Val Pro Lys Lys Ser Val	Ser Ile Met Asp Gly	Ser Asp Glu Gly Ile				
160	165	170				
TTA GCT TGG GTT ACT GTG	AAT TTT CTG ACA GGT	CAG CTG CAT GGC CAC				816
Leu Ala Trp Val Thr Val	Asn Phe Leu Thr Gly	Gln Leu His Gly His				
175	180	185				
AGA CAG GAG ACT GTG GGG	ACC TTG GAC CTA GGG	GGA GCC TCC ACC CAA				864
Arg Gln Glu Thr Val Gly	Thr Leu Asp Leu Gly	Gly Ala Ser Thr Gln				
195	200	205				
ATC ACG TTC CTG CCC CAG	TTT GAG AAA ACT CTG	GAA CAA ACT CCT AGG				912
Ile Thr Phe Leu Pro Gln	Phe Glu Lys Thr Leu	Gln Thr Pro Arg				
210	215	220				
GGC TAC CTC ACT TCC TTT	GAG ATG TTT AAC AGC	ACT TAT AAG CTC TAT				960
Gly Tyr Leu Thr Ser Phe	Glu Met Phe Asn Ser	Thr Tyr Lys Leu Tyr				
225	230	235				

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr 240 245 250	1008
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCG Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Val Gly Phe Glu Pro 290 295 300	1152
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp 320 325 330	1248
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu 335 340 345 350	1296
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu 355 360 365	1344
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr 370 375 380	1392
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val 385 390 395	1440
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGS GCC TTG Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu 400 405 410	1488
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 415 420 425	1539
GTACTTCTTT GGAGACCTGC ATTTGGCAAC ACCTTTTAA GGGGAGSAGA GAGCACTTAG TTTCTGAACT AGTCTGGGAC ATCCTTGACT TGAGCTAGA GATTAGOTT TAATTAATTT TACAAATCTA ATGTGAAGTG CTGCTTAACC ACTCAAGAGT ACACAGCTGG CACGAGAGCA TCACAGAGAG CCCTGTGAGC CAATAAGTAT AGTTTGGAA CTTAACCTTG GAGTGAGAGC CCAGGAGAG GTCCCTGGAA ACCAAGAAA AATCGCATTT CAACCCCTTG AGTGCCCTCAT TCCAGTGAAT ATTTAAATTT TCCTCTTAAA TGTAAAGCTG ACTTATTGCA ATCCCAAGAC CCATCAATAT CAGTATTTTT TTCTTCCCTA TACAGTGCCC TGCCCAACCTT TATCTGCACC CCTCTCCCTT GAAAAGAGA GAAAAAATA AAAAAAATA	1599 1659 1719 1779 1839 1899 1959 1998

Fig. 7 (Cont'd.)

ACR

ACR II

ACR II

ACR II

ACR IV

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CD39L2      485 -----  
CD39L4      429 -----  
CD39L1      432 CRKGTFSHNVVLLCLFSAHFAAGGQGVVILGLPSTI*  
CD39L3      476 ERLPPVPVVGTLAFVALLCLAFATYCSIRKRKEKHAFDRAVD*  
CD39        466 CDSFGSHSGVFPLGFIFVDFEVAQLGLPKPSYFMVMV*
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Fig. 8

FIG. 9